A-11

Gold Cluster Labeling as a New Tool to Study Protein Structures Using Small-angle X-ray Scattering

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A new methodology for using gold cluster labeling as special probes in solution x-ray scattering is presented. Gold cluster labeling provides strong scattering interferences between gold atoms and other atoms. These interferences give the structural information of proteins. We showed how to reconstruct labeled protein structures and extract 1D structural information from solution scattering data. Simulated scattering curves of templates were compared to those of trial structures. The trial structures were built by rigid body modeling (RBM) for a fixed protein with mobile gold cluster(s). Rigid body searches were performed in two steps. First, inter-body distances were estimated from fine-grid RBM without rotation. Secondly, gold center positions were predicted from distance-corrected coarse-grid RBM. Inter-body distances of each trial structure were corrected by least square minimization during RBM. In the analysis, double-labeled and single-labeled data were combined using the best performing scoring function, which improves the prediction accuracy of gold center positions (1.4–8.9 Å error). We also investigated the effect of inter-body distance error and grid error to obtain the nearest neighboring trial structure as a top scoring solution; these trials indicate that 0.2 Å of inter-body distance error and 0.5 Å of grid error are the maximum allowed errors.